

## SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

<120> Peptide-forming enzyme gene, peptide-forming enzyme, and dipeptide  
producing method

<130> PAMA-14174

<150> JP Patent Application 2001-226568

<151> 2001-07-26

<150> JP Patent Application 2001-310547

<151> 2001-10-05

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 30

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1

Thr Lys Thr Leu Gly Ser Leu Gln Leu Glu Glu Ile Thr Leu Thr Leu

1

5

10

15

Pro Leu Thr Glu Asp Val Ala Asp Glu Xaa Arg Xaa Glu Xaa

<210> 2

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:cassette PCR  
primer1

<400> 2

gghwsnytb arytbgarga ratyac

26

<210> 3

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:cassette PCR  
primer2

<400> 3

carytbgarg aratyacbyt bacbytb

27

&lt;210&gt; 4

&lt;211&gt; 1307

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (57)..(1295)

&lt;400&gt; 4

ggcgagctcg ggcagtgggtg ggggtgggtg ccaccctgc gcgtaacctg ggaagc atg 59

Met

1

act aaa aca ctt ggt tcc ctt caa ctt gaa gaa att acc ttg acg ctc 107

Thr Lys Thr Leu Gly Ser Leu Gln Leu Glu Glu Ile Thr Leu Thr Leu

5

10

15

cct ctg act gaa gat gtg gcc gat gaa cgc acc att gat gtg ttc gca 155

Pro Leu Thr Glu Asp Val Ala Asp Glu Arg Thr Ile Asp Val Phe Ala

20

25

30

cgc att gcc aca cgc gtc ggt ggg gaa gac ctt cca tat tta gta ttc 203

Arg Ile Ala Thr Arg Val Gly Gly Glu Asp Leu Pro Tyr Leu Val Phe

35

40

45

ctg cag ggt ggg cct ggc aat gaa gct cca cgt cca agc ctt aat ccc 251

Leu Gln Gly Gly Pro Gly Asn Glu Ala Pro Arg Pro Ser Leu Asn Pro

50

55

60

65

ctc aac ccc aat tgg ttg ggc gtg gcc ttg gag gaa tac cgc gtg gtc 299

Leu Asn Pro Asn Trp Leu Gly Val Ala Leu Glu Glu Tyr Arg Val Val

70

75

80

atg ttg gat caa cgt ggc acc ggc cgt tcc acc cca gtg ggt aat gat 347

Met Leu Asp Gln Arg Gly Thr Gly Arg Ser Thr Pro Val Gly Asn Asp

85

90

95

att ttg gaa aaa ccc aca gca gaa gta gtg gag tac tta tcc cac ctg 395

Ile Leu Glu Lys Pro Thr Ala Glu Val Val Glu Tyr Leu Ser His Leu

100

105

110

cgc gca gat ggc att gtg cga gat gct gaa gcc ctg cgt aag cat ttg 443

Arg Ala Asp Gly Ile Val Arg Asp Ala Glu Ala Leu Arg Lys His Leu

115

120

125

ggt gtg aat cag tgg aac ctt tta ggc cag tcc ttc gga ggt ttc acc 491

Gly Val Asn Gln Trp Asn Leu Leu Gly Gln Ser Phe Gly Gly Phe Thr

130

135

140

145

acc ctg cat tac ttg tcc cgg cac gcc gat tcc ttg gac aac gtg ttt 539

Thr Leu His Tyr Leu Ser Arg His Ala Asp Ser Leu Asp Asn Val Phe

150

155

160

att acc ggc ggt ctc agc gct att gat cgc cca gca gaa gac gtg tat 587

Ile Thr Gly Gly Leu Ser Ala Ile Asp Arg Pro Ala Glu Asp Val Tyr

165

170

175

gcc aac tgt tac aac cgc atg cgc cga aac tct gag gaa ttc tac cgt 635

Ala Asn Cys Tyr Asn Arg Met Arg Arg Asn Ser Glu Glu Phe Tyr Arg

180

185

190

cgc ttc ccg caa tta cgg gaa act ttc cga ggg ttg gtt aat cgt gct 683

Arg Phe Pro Gln Leu Arg Glu Thr Phe Arg Gly Leu Val Asn Arg Ala

195

200

205

cgc gcc ggg gag att gtg ctt ccc acc ggc gaa gtt gtg tca gaa acc 731

Arg Ala Gly Glu Ile Val Leu Pro Thr Gly Glu Val Val Ser Glu Thr

210

215

220

225

agg ctg cga tcc ctt ggt cac ttg ttg ggt agc aat gac ggc tgg ttt 779

Arg Leu Arg Ser Leu Gly His Leu Leu Gly Ser Asn Asp Gly Trp Phe

230

235

240

gat ctg tac aac ctg ctg gaa tta gat ccc acc tcc aac gct ttt gtc 827

Asp Leu Tyr Asn Leu Leu Glu Leu Asp Pro Thr Ser Asn Ala Phe Val

245

250

255

cat gac ctg gca gga ctt ttg cct ttc ggc aac cgc aac cca att tat 875

His Asp Leu Ala Gly Leu Leu Pro Phe Gly Asn Arg Asn Pro Ile Tyr

260

265

270

tac gtg ctc cat gag tcc tct tac gcc gac ggt gtg gtg aca aat tgg 923

Tyr Val Leu His Glu Ser Ser Tyr Ala Asp Gly Val Val Thr Asn Trp

275

280

285

gca gca gag cgt gtg ctt cca gag gat ttc cgc gag gat cca aca ctg 971

Ala Ala Glu Arg Val Leu Pro Glu Asp Phe Arg Glu Asp Pro Thr Leu  
 290 295 300 305

ctc acc ggt gag cac gtg ttc cag gag tgg aca gac acc gtg ccg tcg 1019  
 Leu Thr Gly Glu His Val Phe Gln Glu Trp Thr Asp Thr Val Pro Ser  
 310 315 320

ctc aag ccg tgg aag gac gtt gcc ctg gca ttg gct cag cag gaa tgg 1067  
 Leu Lys Pro Trp Lys Asp Val Ala Leu Ala Leu Ala Gln Gln Glu Trp  
 325 330 335

ccc aag ctt tat gat gcg aag gca ttg gaa aac tca cag gcc aag ggc 1115  
 Pro Lys Leu Tyr Asp Ala Lys Ala Leu Glu Asn Ser Gln Ala Lys Gly  
 340 345 350

gct gca gca gtg tat ghc aat gac gtt ttc gtc cca gtg gat tac tct 1163  
 Ala Ala Ala Val Tyr Xaa Asn Asp Val Phe Val Pro Val Asp Tyr Ser  
 355 360 365

ctg gaa acc gca caa cac ctg ccc ggt gtg cag ctg ttt atc acc agc 1211  
 Leu Glu Thr Ala Gln His Leu Pro Gly Val Gln Leu Phe Ile Thr Ser  
 370 375 380 385

cag cat gaa cac aat gga ctt cgt gcc agc tca ggc gca gta ctg rag 1259  
 Gln His Glu His Asn Gly Leu Arg Ala Ser Ser Gly Ala Val Leu Xaa  
 390 395 400

cac ctt ttc gat ctg gcc cac ggc cga gag gta cgc tgagggcccc cg 1307  
 His Leu Phe Asp Leu Ala His Gly Arg Glu Val Arg

7/26

405

410

<210> 5

<211> 413

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 5

Met. Thr Lys Thr Leu Gly Ser Leu Gln Leu Glu Glu Ile Thr Leu Thr

1 5 10 15

Leu Pro Leu Thr Glu Asp Val Ala Asp Glu Arg Thr Ile Asp Val Phe

20 25 30

Ala Arg Ile Ala Thr Arg Val Gly Gly Glu Asp Leu Pro Tyr Leu Val

35 40 45

Phe Leu Gln Gly Gly Pro Gly Asn Glu Ala Pro Arg Pro Ser Leu Asn

50 55 60

Pro Leu Asn Pro Asn Trp Leu Gly Val Ala Leu Glu Glu Tyr Arg Val

65 70 75 80

Val Met Leu Asp Gln Arg Gly Thr Gly Arg Ser Thr Pro Val Gly Asn

85 90 95

Asp Ile Leu Glu Lys Pro Thr Ala Glu Val Val Glu Tyr Leu Ser His

100 105 110

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Leu Arg Ala Asp Gly Ile Val Arg Asp Ala Glu Ala Leu Arg Lys His  
115 120 125

Leu Gly Val Asn Gln Trp Asn Leu Leu Gly Gln Ser Phe Gly Gly Phe  
130 135 140

Thr Thr Leu His Tyr Leu Ser Arg His Ala Asp Ser Leu Asp Asn Val  
145 150 155 160

Phe Ile Thr Gly Gly Leu Ser Ala Ile Asp Arg Pro Ala Glu Asp Val  
165 170 175

Tyr Ala Asn Cys Tyr Asn Arg Met Arg Arg Asn Ser Glu Glu Phe Tyr  
180 185 190

Arg Arg Phe Pro Gln Leu Arg Glu Thr Phe Arg Gly Leu Val Asn Arg  
195 200 205

Ala Arg Ala Gly Glu Ile Val Leu Pro Thr Gly Glu Val Val Ser Glu  
210 215 220

Thr Arg Leu Arg Ser Leu Gly His Leu Leu Gly Ser Asn Asp Gly Trp  
225 230 235 240

Phe Asp Leu Tyr Asn Leu Leu Glu Leu Asp Pro Thr Ser Asn Ala Phe  
245 250 255

Val His Asp Leu Ala Gly Leu Leu Pro Phe Gly Asn Arg Asn Pro Ile



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260

265

270

Tyr Tyr Val Leu His Glu Ser Ser Tyr Ala Asp Gly Val Val Thr Asn  
275 280 285

Trp Ala Ala Glu Arg Val Leu Pro Glu Asp Phe Arg Glu Asp Pro Thr  
290 295 300

Leu Leu Thr Gly Glu His Val Phe Gln Glu Trp Thr Asp Thr Val Pro  
305 310 315 320

Ser Leu Lys Pro Trp Lys Asp Val Ala Leu Ala Leu Ala Gln Gln Glu  
325 330 335

Trp Pro Lys Leu Tyr Asp Ala Lys Ala Leu Glu Asn Ser Gln Ala Lys  
340 345 350

Gly Ala Ala Ala Val Tyr Xaa Asn Asp Val Phe Val Pro Val Asp Tyr  
355 360 365

Ser Leu Glu Thr Ala Gln His Leu Pro Gly Val Gln Leu Phe Ile Thr  
370 375 380

Ser Gln His Glu His Asn Gly Leu Arg Ala Ser Ser Gly Ala Val Leu  
385 390 395 400

Xaa His Leu Phe Asp Leu Ala His Gly Arg Glu Val Arg  
405 410

10/26

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 6

ggcagctcg ggcagtgggtg ggggtgggtg

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<210> 7

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 7

cgggggccct cagcgtacct ctcggccgtg

30

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 8

ggcgagctca tgactaaaac acttggttcc

30

<210> 9

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 9

ggcggatccg gtgctcaaag cgcaa

25

<210> 10

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 10

12/26

ggcggatcag gtcgccggt tcttc

25

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 11

cacgcgctgc agcaaaccoc tcat

24

<210> 12

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 12

cccgaattct tacggagcgc gcaatg

26

<210> 13

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 13

cggggatccc ttcattgcttc ttcagg

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<210> 14

<211> 2078

<212> DNA

<213> Pseudomonas putida

<220>

<221> CDS

<222> (486)..(1496)

<400> 14

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ttggctatgc cctgttgttg gatgccact cgatccgctc gcacatcccg cacctgttcg 120

atggcaagtt gccggacttc aacctgggta ccttcaatgg cgccagctgc gatccggtgc 180

tggccgagcg gttgcagggc gtgtgcgccg aagcgacagg ttacagtcac gtgttgaatg 240

gtcgggtcaa aggcggacac atcaccggcg actatggtga ccccggaag catatccatg 300

cggtgcagct ggagttggcg caaagcacgt acatggagga aaccgagccg ttacctacc 360

gggaagacct ggcgcaaccg acgcaggtgg ttctgaagca gcttttgcaa gcgctgctgg 420

cttggggggc agaacgatac cagcgttgag tggaagaggc ggtgctcaaa gcgcaattca 480

ggttt atg atg ccc aac ggc agt caa tat cct cac acg gag tgc gca atg 530

Met Met Pro Asn Gly Ser Gln Tyr Pro His Thr Glu Cys Ala Met

1

5

10

15

cag acc ctc tac ccg cag atc aaa ccc tac gcc cgg cac gat ctg gcc 578

Gln Thr Leu Tyr Pro Gln Ile Lys Pro Tyr Ala Arg His Asp Leu Ala

20

25

30

gtg gaa gcg ccg cat gtg ctg tat gtc gat gaa agc ggc tcg ccg gaa 626

Val Glu Ala Pro His Val Leu Tyr Val Asp Glu Ser Gly Ser Pro Glu

35

40

45

ggt ctg ccc gtg gta ttc atc cac ggt ggc ccg ggt gct ggc tgc gac 674

Gly Leu Pro Val Val Phe Ile His Gly Gly Pro Gly Ala Gly Cys Asp

50

55

60

gcc cag agc cgt tgc tac ttt gac ccc aac ctg tac cgc atc atc acc 722

Ala Gln Ser Arg Cys Tyr Phe Asp Pro Asn Leu Tyr Arg Ile Ile Thr

65

70

75

ttc gac cag cgc ggc tgt ggc cgc tcc acg ccc cat gcc agc ctg gag 770

Phe Asp Gln Arg Gly Cys Gly Arg Ser Thr Pro His Ala Ser Leu Glu

80	85	90	95
aac aac aca acc tgg cac ctg gtc gag gac ctg gag cgc atc cgc gag 818			
Asn Asn Thr Thr Trp His Leu Val Glu Asp Leu Glu Arg Ile Arg Glu			
100	105	110	
cac ctg ggc atc gac aaa tgg gtg ctg ttc ggc ggc tcg tgg ggt tcg 866			
His Leu Gly Ile Asp Lys Trp Val Leu Phe Gly Gly Ser Trp Gly Ser			
115	120	125	
acc ctg gcc ctg gcc tac gcc cag acc cac ccc gag cgt gtg cat ggg 914			
Thr Leu Ala Leu Ala Tyr Ala Gln Thr His Pro Glu Arg Val His Gly			
130	135	140	
ctg atc ctg cgg ggc atc ttc ctg tgc cgg ccg cag gag atc gag tgg 962			
Leu Ile Leu Arg Gly Ile Phe Leu Cys Arg Pro Gln Glu Ile Glu Trp			
145	150	155	
ttc tac cag gag ggc gcc agc cgc ctg ttc ccc gac tac tgg cag gac 1010			
Phe Tyr Gln Glu Gly Ala Ser Arg Leu Phe Pro Asp Tyr Trp Gln Asp			
160	165	170	175
tac atc gcg ccg att ccg ccg gaa gaa cgc ggc gac ctg gtc aag gcc 1058			
Tyr Ile Ala Pro Ile Pro Pro Glu Glu Arg Gly Asp Leu Val Lys Ala			
180	185	190	
ttc cac aag cgc ctc acc ggt aac gat cag att gcc cag atg cac gcc 1106			
Phe His Lys Arg Leu Thr Gly Asn Asp Gln Ile Ala Gln Met His Ala			
195	200	205	

gcc aag gcg tgg tct acc tgg gag ggc cgt acc gcc acc ctg cgc ccg 1154

Ala Lys Ala Trp Ser Thr Trp Glu Gly Arg Thr Ala Thr Leu Arg Pro

210

215

220

aac ccg ctg gtg gtc gac cgc ttc tcc gag ccg cag cgg gcg ctg tcg 1202

Asn Pro Leu Val Val Asp Arg Phe Ser Glu Pro Gln Arg Ala Leu Ser

225

230

235

atc gcc cgg atc gag tgc cac tac ttc atg aac aac gcc ttc ctc gaa 1250

Ile Ala Arg Ile Glu Cys His Tyr Phe Met Asn Asn Ala Phe Leu Glu

240

245

250

255

ccg gac cag ttg atc cgc gac ctg ccg aag atc gcc cac ctg cca gcg 1298

Pro Asp Gln Leu Ile Arg Asp Leu Pro Lys Ile Ala His Leu Pro Ala

260

265

270

gtg atc gtg cac ggt cgc tat gac gtg atc tgt ccg ctg gac aac gcc 1346

Val Ile Val His Gly Arg Tyr Asp Val Ile Cys Pro Leu Asp Asn Ala

275

280

285

tgg gcc ctg cac cag gcc tgg ccg aac agc gaa ctg aag gtg atc cgc 1394

Trp Ala Leu His Gln Ala Trp Pro Asn Ser Glu Leu Lys Val Ile Arg

290

295

300

gac gcc ggc cac gcc gcg tcc gag ccg ggc atc acc gat gcc ctg gtg 1442

Asp Ala Gly His Ala Ala Ser Glu Pro Gly Ile Thr Asp Ala Leu Val

305

310

315



17/26

cgg gca gcc gac cag atg gcc cgg cgc ctg ctc gac ctg ccc ctg gaa 1490

Arg Ala Ala Asp Gln Met Ala Arg Arg Leu Leu Asp Leu Pro Leu Glu

320

325

330

335

gaa gca tgaggggttt gctgcagcgc gtgcgcggtg cgcgggttga agtggcgggg 1546

Glu Ala

caggtggttg gcgcgatcga ccagggtttg ctggtgctgg tggccgtcga gcctgaagat 1606

tcccgcgagc aggccgataa gctgttgac aagctgctga actaccgtgt attcagcgat 1666

gagcacggca agatgaacct gtcgctcaag gatgtcgggg gtggtttgtt gctggtgtcg 1726

cagttcacct tggcggcgga caccgcaac ggcatgcgtc cgagcttctc gacggcagcg 1786

ccgccggccc tcggggctga attgttcgac tatcttttgc agcaagcgaa gcgccagcat 1846

gccgacgtgg cgagcgggca attcggggca gacatgcagg tgcacttggt caatgatggc 1906

ccgtaacat ttatgttaca aatatgaggt caaaaaaccc tttgtttata ggaaaacaag 1966

gggttttgta cgataaatag ttgttccagc ctgatgcgtt gtcacgcgac ctgctggata 2026

atcgcgcgct gcatggacct gcgttcgcag gttcgtttca ctctgactcg ag 2078

<210> 15

<211> 337

<212> PRT

<213> *Pseudomonas putida*

&lt;400&gt; 15

Met Met Pro Asn Gly Ser Gln Tyr Pro His Thr Glu Cys Ala Met Gln  
 1                    5                    10                    15

Thr Leu Tyr Pro Gln Ile Lys Pro Tyr Ala Arg His Asp Leu Ala Val  
                   20                    25                    30

Glu Ala Pro His Val Leu Tyr Val Asp Glu Ser Gly Ser Pro Glu Gly  
                   35                    40                    45

Leu Pro Val Val Phe Ile His Gly Gly Pro Gly Ala Gly Cys Asp Ala  
                   50                    55                    60

Gln Ser Arg Cys Tyr Phe Asp Pro Asn Leu Tyr Arg Ile Ile Thr Phe  
                   65                    70                    75                    80

Asp Gln Arg Gly Cys Gly Arg Ser Thr Pro His Ala Ser Leu Glu Asn  
                   85                    90                    95

Asn Thr Thr Trp His Leu Val Glu Asp Leu Glu Arg Ile Arg Glu His  
                   100                    105                    110

Leu Gly Ile Asp Lys Trp Val Leu Phe Gly Gly Ser Trp Gly Ser Thr  
                   115                    120                    125

Leu Ala Leu Ala Tyr Ala Gln Thr His Pro Glu Arg Val His Gly Leu  
                   130                    135                    140

Ile Leu Arg Gly Ile Phe Leu Cys Arg Pro Gln Glu Ile Glu Trp Phe  
 145 150 155 160

Tyr Gln Glu Gly Ala Ser Arg Leu Phe Pro Asp Tyr Trp Gln Asp Tyr  
 165 170 175

Ile Ala Pro Ile Pro Pro Glu Glu Arg Gly Asp Leu Val Lys Ala Phe  
 180 185 190

His Lys Arg Leu Thr Gly Asn Asp Gln Ile Ala Gln Met His Ala Ala  
 195 200 205

Lys Ala Trp Ser Thr Trp Glu Gly Arg Thr Ala Thr Leu Arg Pro Asn  
 210 215 220

Pro Leu Val Val Asp Arg Phe Ser Glu Pro Gln Arg Ala Leu Ser Ile  
 225 230 235 240

Ala Arg Ile Glu Cys His Tyr Phe Met Asn Asn Ala Phe Leu Glu Pro  
 245 250 255

Asp Gln Leu Ile Arg Asp Leu Pro Lys Ile Ala His Leu Pro Ala Val  
 260 265 270

Ile Val His Gly Arg Tyr Asp Val Ile Cys Pro Leu Asp Asn Ala Trp  
 275 280 285

Ala Leu His Gln Ala Trp Pro Asn Ser Glu Leu Lys Val Ile Arg Asp

290

295

300

Ala Gly His Ala Ala Ser Glu Pro Gly Ile Thr Asp Ala Leu Val Arg

305

310

315

320

Ala Ala Asp Gln Met Ala Arg Arg Leu Leu Asp Leu Pro Leu Glu Glu

325

330

335

Ala

<210> 16

<211> 1360

<212> DNA

<213> *Pseudomonas putida*

<220>

<221> CDS

<222> (311)..(1279)

<400> 16

ctggaagggt tcttggcgtg gggccagaag cactacacct gagtcaacga ggatcaaaat 60

gtgggagcgg gcttgtcagg tcgccgcata gccgcgatgg cggctctgtca gttcccaata 120

tgtcgactga tccgccgcta tcgcgagcaa gcccgctccc acacgtggtg cgcgaacctt 180

cctggctgat cactgacaca ggtctaagtc ctcaaggaca tgctcattgc acaattcggg 240

tttatgatgc cagacggcaa aataatagac gtccccccag ggatggaccc gacccttac 300

ggagcgcgca atg cag act ttg tac ccg cag atc aaa ccc tac gtc cgg 349

Met Gln Thr Leu Tyr Pro Gln Ile Lys Pro Tyr Val Arg

1

5

10

cac gat ctg gcc gtc gat gaa acc cac acg ctg tat gtc gac gaa agt 397

His Asp Leu Ala Val Asp Glu Thr His Thr Leu Tyr Val Asp Glu Ser

15

20

25

ggt tcc ccg caa ggt ttg ccc gtg gtc ttc atc cat ggc ggt ccc ggc 445

Gly Ser Pro Gln Gly Leu Pro Val Val Phe Ile His Gly Gly Pro Gly

30

35

40

45

gcc ggc tgc gat gcc aat agc cgc tgc tat ttc gat ccg aac ctg tac 493

Ala Gly Cys Asp Ala Asn Ser Arg Cys Tyr Phe Asp Pro Asn Leu Tyr

50

55

60

cgc atc gtc acc ttt gac cag cgc ggc tgc ggg cgc tcc act ccg cgg 541

Arg Ile Val Thr Phe Asp Gln Arg Gly Cys Gly Arg Ser Thr Pro Arg

65

70

75

gcc agc ctg gaa aac aac acc acc tgg gac ctg gtt gcc gac ctt gag 589

Ala Ser Leu Glu Asn Asn Thr Thr Trp Asp Leu Val Ala Asp Leu Glu

80

85

90

cgc att cgc gag cac ctg ggg att gaa aaa tgg gtg ctg ttc ggt ggt 637

Arg Ile Arg Glu His Leu Gly Ile Glu Lys Trp Val Leu Phe Gly Gly

95

100

105

tcc tgg ggc tgc acc ctg gcc ctg gcc tat gca caa acc cac cct gat 685

Ser Trp Gly Ser Thr Leu Ala Leu Ala Tyr Ala Gln Thr His Pro Asp

110

115

120

125

cgc gtg ctt ggc ctg att gtg cgc ggc atc ttc ctg gcc cgc ccc cag 733

Arg Val Leu Gly Leu Ile Val Arg Gly Ile Phe Leu Ala Arg Pro Gln

130

135

140

gat atc cag tgg ttc tac cag gcc ggc gcg agc cgc ctg ttc ccg gac 781

Asp Ile Gln Trp Phe Tyr Gln Ala Gly Ala Ser Arg Leu Phe Pro Asp

145

150

155

tac tgg cag gac tac atc gcg cca atc ccg gcg gaa gag cgc cac gac 829

Tyr Trp Gln Asp Tyr Ile Ala Pro Ile Pro Ala Glu Glu Arg His Asp

160

165

170

atg atc agc gcc tac cac aag cgc ctg acc ggc aat gac cag atc gcc 877

Met Ile Ser Ala Tyr His Lys Arg Leu Thr Gly Asn Asp Gln Ile Ala

175

180

185

cag atg cat gcc gcc aag gcc tgg tcc acc tgg gaa ggc cgc atg ctc 925

Gln Met His Ala Ala Lys Ala Trp Ser Thr Trp Glu Gly Arg Met Leu

190

195

200

205

ggc ctg tgc ccc agc ccg cag ctg atc gag cgc ttc tcc gag ccc cag 973

Gly Leu Cys Pro Ser Pro Gln Leu Ile Glu Arg Phe Ser Glu Pro Gln

210	215	220	
cgc gcg ttg tcg att gcg cgc atc gag tgc cac tac ttc acc aat aac			1021
Arg Ala Leu Ser Ile Ala Arg Ile Glu Cys His Tyr Phe Thr Asn Asn			
225	230	235	
tcg ttc ctg gag ccc aac cag ctg att cgc gat atg cac aag atc gcc			1069
Ser Phe Leu Glu Pro Asn Gln Leu Ile Arg Asp Met His Lys Ile Ala			
240	245	250	
cat ctg ccg ggg atc atc gtg cat ggc cgc tac gat atg atc tgc ccg			1117
His Leu Pro Gly Ile Ile Val His Gly Arg Tyr Asp Met Ile Cys Pro			
255	260	265	
ctg gat aat gcc tgg gag ctg cac cag gcc tgg ccg aac agt gag ttg			1165
Leu Asp Asn Ala Trp Glu Leu His Gln Ala Trp Pro Asn Ser Glu Leu			
270	275	280	285
cag gtg atc cgc gag gcg ggc cac gcg gcg tcc gag ccg ggc atc acc			1213
Gln Val Ile Arg Glu Ala Gly His Ala Ala Ser Glu Pro Gly Ile Thr			
290	295	300	
gat gcg ctg gtg cgt gcg gcg ggc gat atg gca cga cgc ctg ctt gat			1261
Asp Ala Leu Val Arg Ala Ala Gly Asp Met Ala Arg Arg Leu Leu Asp			
305	310	315	
ctg ccc cct gaa gaa gca tgaagggcct ttttgccnna cgggtgcgtg			1309
Leu Pro Pro Glu Glu Ala			
320			

gcgccgggtc agtggcgggc aagtgggtggg cgcatagac cagggttgca g 1360

<210> 17

<211> 323

<212> PRT

<213> Pseudomonas putida

<400> 17

Met Gln Thr Leu Tyr Pro Gln Ile Lys Pro Tyr Val Arg His Asp Leu

1 5 10 15

Ala Val Asp Glu Thr His Thr Leu Tyr Val Asp Glu Ser Gly Ser Pro

20 25 30

Gln Gly Leu Pro Val Val Phe Ile His Gly Gly Pro Gly Ala Gly Cys

35 40 45

Asp Ala Asn Ser Arg Cys Tyr Phe Asp Pro Asn Leu Tyr Arg Ile Val

50 55 60

Thr Phe Asp Gln Arg Gly Cys Gly Arg Ser Thr Pro Arg Ala Ser Leu

65 70 75 80

Glu Asn Asn Thr Thr Trp Asp Leu Val Ala Asp Leu Glu Arg Ile Arg

85 90 95

Glu His Leu Gly Ile Glu Lys Trp Val Leu Phe Gly Gly Ser Trp Gly



100

105

110

Ser Thr Leu Ala Leu Ala Tyr Ala Gln Thr His Pro Asp Arg Val Leu

115

120

125

Gly Leu Ile Val Arg Gly Ile Phe Leu Ala Arg Pro Gln Asp Ile Gln

130

135

140

Trp Phe Tyr Gln Ala Gly Ala Ser Arg Leu Phe Pro Asp Tyr Trp Gln

145

150

155

160

Asp Tyr Ile Ala Pro Ile Pro Ala Glu Glu Arg His Asp Met Ile Ser

165

170

175

Ala Tyr His Lys Arg Leu Thr Gly Asn Asp Gln Ile Ala Gln Met His

180

185

190

Ala Ala Lys Ala Trp Ser Thr Trp Glu Gly Arg Met Leu Gly Leu Cys

195

200

205

Pro Ser Pro Gln Leu Ile Glu Arg Phe Ser Glu Pro Gln Arg Ala Leu

210

215

220

Ser Ile Ala Arg Ile Glu Cys His Tyr Phe Thr Asn Asn Ser Phe Leu

225

230

235

240

Glu Pro Asn Gln Leu Ile Arg Asp Met His Lys Ile Ala His Leu Pro

245

250

255

26/26

Gly Ile Ile Val His Gly Arg Tyr Asp Met Ile Cys Pro Leu Asp Asn

260

265

270

Ala Trp Glu Leu His Gln Ala Trp Pro Asn Ser Glu Leu Gln Val Ile

275

280

285

Arg Glu Ala Gly His Ala Ala Ser Glu Pro Gly Ile Thr Asp Ala Leu

290

295

300

Val Arg Ala Ala Gly Asp Met Ala Arg Arg Leu Leu Asp Leu Pro Pro

305

310

315

320

Glu Glu Ala